M. R. Pollock
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Medical Research Council
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Dear Pollock:

Thank you very much for your letter of October 16. The results on the penicillin system are as surprising as they are exciting. One would not have guessed a priori that such a small number of molecules would be adequate for maximal adaptation. I wonder whether you already have available the information which would tell us how many molecules can actually be fixed by an inadapted cell. This information might enable one to make some estimation of the number of active sites. It is possible that you are dealing with a situation in which the enzyme-forming system preexists and what you are following is essentially enzyme formation. It is undoubtedly fortuitous that the number 100 is of the same order of magnitude as our estimation of the number of discrete enzyme-forming elements.

In answer to the question which you raise, I am afraid that I don't have any scheme for visualizing how our particles function in promoting enzyme synthesis. We have recently been able to demonstrate fairly conclusively with the maltose system that no complex protein precursor exists which can be converted into active enzyme without the participation of the free amino acid pool of the cell. While our results cannot eliminate the involvement of a complex precursor, they do make it necessary to postulate primary peptide bond formation as a necessary stage. They suggest that complex precursors are broken down to their constituent amino acids and enzyme formation proceeds from scratch at this level. As you can well imagine, this result was something of a surprise to us and makes it even less likely that we will be in a position in the immediate future of visualizing a mechanism for enzyme synthesis.

At the present time, I am planning to attend the Congress in Paris next year. Unless unforeseen difficulties arise between now and next summer, I anticipate getting together with you for an extended discussion.

Sincerely yours,

S. Spiegelman

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